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(54) Title: RESTRICTION ENZYME SCREEN FOR DIFFERENTIATING PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS STRAINS			
(57) Abstract <p>A test based on restriction enzyme analysis identifies and differentiates strains of porcine reproductive and respiratory syndrome virus (PRRSV). Amplified cDNA from the ORF 5 region of the viral genome has been targeted for identification of unique restriction sites that allow for the differentiation of the vaccine strain from field strains, and for differentiation of field strains from each other through the use of selected restriction enzymes. This assay is useful for both clinical diagnosis of PRRSV field strains in vaccinated pigs as well as for epidemiological studies in the evaluation of the source and transmission of PRRS field viruses.</p>			

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**RESTRICTION ENZYME SCREEN FOR DIFFERENTIATING PORCINE
REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS STRAINS**

Background of the Invention

Field of the Invention

This invention relates to a differential test for distinguishing strains of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from one another and for differentiating field stains from the currently used vaccine strain.

Porcine reproductive and respiratory syndrome (PRRS) was first reported in North America in 1987 (Keffaber, 1989) and emerged in Europe in late 1990 (Wensvoort et al., 1991). Recently, PRRS has gained world-wide attention because of its economic impact on the swine industry. The disease is characterized by reproductive failure in pregnant sows and respiratory problems in pigs of all ages (Loula, 1991). The causative agent of PRRS is a small (50-60nm) positive-stranded RNA enveloped virus. The genome is a polyadenylated RNA molecule of about 15 kb and contains eight open reading frames (ORFs). Viral proteins are expressed by six subgenomic mRNAs which are transcribed from the negative strand using a body sequence derived from the 5' end of the viral genome (Meulenbergh et al., 1995). The virus replicase is most likely encoded by ORFs 1a/1b by a -1 frameshift (Conzelmann et al., 1993). Open reading frames 2 to 4 encode for putative structural proteins (Van Nieuwstadt, 1995). ORF 5 encodes for a envelope (E) glycoprotein of approximately 25 kDa. A non-glycosylated membrane (M) protein of 18 kDa is encoded by ORF 6 and the nucleocapsid (N) protein of 15 kDa is encoded by ORF 7 (Meulenbergh et al., 1995; Conzelmann et al., 1993).

Morphologically and morphogenetically, PRRSV resembles equine arteritis virus (EAV), lactate dehydrogenase-elevating

virus (LDV), and simian hemorrhagic fever virus (SHFV) (Conzelmann et al., 1993; Meulenberge et al., 1993; Plagemann and Moennig, 1991; Snijder and Spaan, 1995). As a result of common features shared by these viruses, they have been tentatively grouped into a new virus family, Arteriviridae (Conzelmann et al., 1993; Meulenberge et al., 1993, Plagemann and Moennig, 1992).

Description of the Prior Art

Although the clinical features of PRRS in the United States and in Europe appear similar, several recent studies have indicated phenotypic, antigenic, and genetic differences exist among PRRSV isolates (Bautista et al., 1993; Meng et al., 1994; Wensvoort et al., 1992). The amino acid sequences of ORF 2 through ORF 7 of North American isolates share only 55-79% homology with those of European descent (Meulenberge et al., 1995). It is believed that the glycosylated structural envelope protein E, encoded by ORF 5, is partially responsible for these serological variations among isolates of PRRSV (Meulenberge et al., 1995). Protein E is the counterpart of G_L of EAV (de Vries et al., 1992) and VP-3 of LDV (Gogeny et al., 1993). Both (G_L and E) proteins contain a large internal hydrophobic region which has been thought to anchor these proteins in the membrane (Meulenberge et al., 1995). The existence of neutralizing epitopes in VP-3 of LDV (Harty and Plagemann, 1988) and G_L of EAV (Balasuriya et al., 1995) was demonstrated using monoclonal antibodies and sequencing escape mutants. More recent studies indicate that protein E plays a role in inducing neutralizing antibodies (Pesch et al., 1995).

A modified-live-virus vaccine strain RespPRRS® of PPRSV is currently used in the United States for the prevention of the respiratory facet of the syndrome. Although the vaccine strain

is attenuated, it, like virulent field strains of PRRSV, has the ability to persist for at least several weeks in a vaccinated pig. Consequently, the source of PRRSV isolated from diagnostic samples is sometimes in question and it would be highly desirable to have a positive assay for identifying the source.

Summary of the Invention

We have now discovered that ORF 5 can be targeted in a restriction enzyme analysis for distinguishing vaccine strain RespPRRS® of PRRSV from virulent field strains and also for distinguishing field strains from one another. The reading frame is first converted to a double stranded DNA, amplified, and then cut with restriction enzymes in conserved regions which collectively have sufficient variability among strains to permit generation of a unique fragment profile for each strain of PRRSV.

In accordance with this discovery, it is an object of the invention to provide a tool for distinguishing vaccine strain RespPRRS® from wild-type field strains.

It is also an object of the invention to provide a tool for epidemiological studies in the evaluation of the source and transmission of field strains of PRRSV.

It is also an object of the invention to provide a sensitive, reliable, and rapid assay for PRRSV suitable for large-scale herd screening.

A further object of the invention is to provide a diagnostic basis for designing an effective control program for PRRS in swine herds.

Other objects and advantages of this invention will become readily apparent from the ensuing description.

Brief Description of the Drawing

FIG. 1 shows the aligned ORF 5 sequences for field strain VR 2332 and vaccine strain RespPRRS® of PRRSV as well as the consensus sequence for these strains.

FIG. 2 shows the aligned ORF 5 nucleotide sequences for the 22 field strains and strain RespPRRS® of PRRSV sequenced in conjunction with the invention, and for strain VR 2332 (previously sequenced by others) as compared to the consensus sequence.

FIG. 3 is a computer generated schematic diagram of *Mlu I*, *Sfc I*, *Hinc II* and *Sac II* ORF 5 cDNA fragments for PRRSV field strain NADC-8 (F) and vaccine strain RespPRRS® (V).

Detailed Description of the Invention

The primary points of novelty regarding the identification and distinction of individual strains of PRRSV in accordance with this invention include: (1) identification of a segment of the viral genome that is sufficiently variable among strains to allow differentiation, yet stable enough so that there is a low probability of mutational changes during repeated *in vitro* or *in vivo* passages of a particular strain; (2) selection of a universal set of primers that allows for reverse transcription (RT) and polymerase chain reaction (PCR) amplification of this segment; and (3) identification of unique restriction sites that allow for the differentiation of vaccine strains from field strains, and field strains from one another.

Insofar as currently known, ORF 5 is the only region of the PRRSV genome that has the proper combination of nucleotide variability among strains of PRRSV (exemplified by those listed in Table I) together with long term stability to allow for restriction enzyme differentiation. On the other hand, the stability of the ORF 5 nucleotide sequence of a particular

strain is indicated (FIG. 1) by the fact that there are only two base differences (positions 38 and 451) between vaccine strain RespPRRS® (indicated in the figure as "resp.PRRS"), which was attenuated by repeated serial passages in cell culture, and its presumed parental strain VR 2332. These two strains (which could be considered variations of the same strain) are indistinguishable on the basis of restriction patterns associated with any of the 77 restriction enzymes reported in Table II.

FIG. 2 clearly depicts variations in the ORF 5 nucleotide sequences for strain RespPRRS® of PRRSV sequenced in conjunction with the invention and for 23 field strains of PRRSV, including 22 field strains sequenced in conjunction with the invention and VR 2332 (the sequence of which was previously reported in the literature). The consensus sequence for the 24 strains is also given in the figure. The position and frequency of these variations are sufficient to permit differentiation of every field strain (except presumed parental strain VR 2332) from the vaccine strain using a singular enzyme, either *Mlu* I or *Sfc* I (see Tables I and II). Assaying with both enzymes provides confirmation. As best shown in Table I, a high degree of assurance can be obtained by comparing the combined fragment patterns from *Mlu* I, *Sfc* I, *Hinc* II, and *Sac* II. All 23 of the field strains in Table I can be differentiated from one another by means of an appropriate combination of six or fewer restriction enzymes selected by reference to Table II. In Table II, the PRRSV strains are shown across the top and 77 enzymes which were evaluated for purposes of the invention are indicated on the left. The last column represents the cut sites for both strain RespPRRS® and its presumed parental strain VR 2332. Even though there are two base differences between the ORF 5 of these two strains, the cutting sites in the respective ORF 5 cDNAs are

the same for all of the 77 enzymes shown in the table. The numbers shown in the table cells represent the size of the resultant fragments obtained by cutting a 716 bp amplified DNA including the ORF 5. Multiple fragment sizes are listed in order from 5' to 3'. The symbol "xxx" indicates that the particular enzyme does not cleave anywhere within the 716 bp fragment.

Given that the PRRSV genome is RNA, the region coding for ORF 5 must first be reverse transcribed by methods known in the art to produce double stranded cDNA. By means of PCR or any other like process, the coding region is then amplified to the extent necessary for the subsequent restriction enzyme analysis.

Primers are preferably selected from nearby flanking regions upstream and downstream from the reading frame.

Example 1

Cell and Virus Propagation.

MARC-145 cells (Kim et al., 1993, herein incorporated by reference) were cultured in Eagle's minimum essential medium (MEM), supplemented with 5% fetal bovine serum (FBS) and antibiotics. Twenty-two field stains of PRRSV isolated from Canada, Guatemala, and the United States as well as vaccine strain RespPRRS® of PPRSV were propagated and then cloned by three rounds of end point dilutions on MARC-145.

RNA extraction and Reverse Transcriptase Polymerase Chain Reaction.

Viral RNA was isolated from 22 field strains and vaccine strain RespPRRS® of PRRSV (see Table I) using a standard guanidinium isothiocyanate method (Sambrook et al., 1989, herein incorporated by reference). Single tube reverse transcriptase polymerase chain reactions (RT-PCR) as described by Sellner et

al. (1992, herein incorporated by reference) with slight modifications were conducted on RNA isolated from each of the 23 strains in a Perkin-Elmer 4800®. Primers were designed based on the nucleotide sequence of field strain VR 2385 (Meng et al., 1995; Morozov et al., 1995, both herein incorporated by reference) and synthesized by Integrated DNA Technologies, Inc. (Coralville, IA). The sense primer was 5'-CCATTCTGTTGGCAATTGTA-3' (SEQ ID NO:25) and the anti-sense primer was 5'-GGCATATATCATCACTGGCG-3' (SEQ ID NO:26). In SEQ ID NO:27 (which is similar to SEQ ID NO:23 for ORF 5 of vaccine virus RespPRRS but additionally shows the immediate flanking regions), the sense primer extends from nucleotide 1 through nucleotide 20 and the antisense primer is the complement to the nucleotide sequence extending from nucleotide 716 to 697. A 716 bp piece encompassing ORF 5, with flanking regions of ORF 4 and ORF 6, was generated for all strains and the fragments were purified using a GENECLEAN® kit (Bio 101).

sequencing.

Double stranded nucleotide sequencing (Tabor and Richardson, 1987, herein incorporated by reference) with Taq polymerase and fluorescently labelled dideoxynucleotides (Applied Biosystems International, Prism System) as described in Sanger et al. (1977, herein incorporated by reference) was performed in triplicate on both strands for analysis with an Applied Biosystems 373A® automated sequencer. The same primer set as described above was used for sequencing. Nucleotide sequence editing and alignments were performed using Intelligenetics, GENEWORKS® version 2.2 software.

Analysis.

To determine the rate of possible drift of ORF 5 sequence, four PRRSV strains of U.S. origin: NADC-8, NADC-9, 41572-2, and 18310-A were repeatedly passed on MARC-145 cells. NADC-8, NADC-9, and 41572-2 encountered 61 passages, and 18310 encountered 31 passages. RT-PCR was performed and the subsequent product was sequenced as described above.

Sequencing of the four selected strains passed in vitro revealed: 6 nucleotide and 4 amino acid substitutions (2,110,136,194 a.a.) for NADC-8; 2 nucleotide and 1 amino acid substitution (59 a.a.) for NADC-9; 2 nucleotide and 2 amino acid substitutions (3, 34 a.a.) for strain 41572-2; and 4 nucleotide and 2 amino acid substitutions (3,194 a.a.) for strain 18310-A (data not shown). However, none of these changes affected restriction patterns of any of these four strains.

Comparison of Sequences.

The complete ORF 5 gene sequence for each of 22 PRRSV field strains and for the vaccine strain RespPRRS® was determined. The sequences for the field strains are shown in the SEQUENCE LISTING as SEQ ID NOS:1-22, that for field strain VR 2332 (previously published) is shown as SEQ ID NO:23, and that for vaccine strain RespPRRS® is shown as SEQ ID NO:24. These sequences were aligned and compared (FIG. 2) to the consensus sequence for all 24 strains. Alignment analysis indicates the same initiation and termination sites exist for all 24 strains. Regions of high and low variability are also apparent. Insertions and deletions were found to be nonexistent on the nucleotide level.

Example 2

To differentiate the vaccine strain RespPRRS® and the presumed parental field strain VR 2332 from the 22 remaining (field) strains shown in Table I, it was necessary to select one or more appropriate restriction enzymes. The selection was based on a comparison of the ORF 5 sequence data for these stains in conjunction with the known cut sites for the enzymes as summarized in Table II. Using this technique, enzymes *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II were initially selected. The enzymes *Mlu* I and *Sfc* I cut only the vaccine strain RespPRRS® and field strain VR 2332, and do not cut any of the other 22 PRRSV strains shown in Tables I and II. The restriction enzymes *Hinc* II and *Sac* II cut most of the PRRSV strains tested giving various gel patterns. Only strains 4 and 9 have a *Hinc* II gel pattern identical to the RespPRRS®/VR 2332 gel pattern. A second gel analysis with *Sac* II differentiates the vaccine strain and VR 2332 from PRRSV field strains 4 and 9. The combined results with the 4 restriction enzymes give a high degree of assurance of the RespPRRS®/VR 2332 genotype.

Restriction enzymes *Mlu* I and *Sfc* I are particularly valuable for differentiation because these enzymes cut only strain RespPRRS®/VR 2332 and none of the other 22 strains of PRRSV. *Mlu* I recognizes the 6 base pair sequence A'CGCGT. For the other 22 PRRSV strains, there are two base differences, namely, guanines at positions 409 and 411; both need to occur in order to create a functional *Mlu* I site. Since two bases need to change for the other strains of PRRSV, the *Mlu* I pattern is a strong marker for the RespPRRS®/VR 2332 genotype. Also *Sfc* I only cuts the RespPRRS®/VR 2332 PCR-amplified DNA fragment. However, 9 of the 22 other strains of PRRSV require only a single nucleotide change, in the localized 6-nucleotide cutting site, to create a functional *Sfc* I site. Therefore, mutations

resulting in *Sfc* I cutting are potentially more frequent than those for *Mlu* I cutting. As a safeguard against erroneous identification resulting from such mutations, it is advisable to conduct the assay with additional enzymes.

A typical gel electrophoresis test, in which vaccine strain RespPRRS® and strain NADC 8 are compared after digestion with *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II, is represented by FIG. 3. The *Mlu* I and *Sfc* I gel patterns of strain NADC 8 are the same for all 22 PRRSV strains and distinct from strain RespPRRS®/VR 2332 gel pattern. For restriction enzymes *Hinc* II and *Sac* II, strain NADC-8 gel patterns are also distinct from strain RespPRRS®/VR 2332 patterns, but similar to other PRRSV strains. However, all of the PRRSV strains in Table II can be differentiated one from another by appropriate selection of restriction enzymes. No more than 6 restriction enzymes would be needed for differentiating the strains reported in Table II.

Example 3

The constancy of the restriction enzyme pattern within ORF 5 during persistent infection of pigs with PRRSV was evaluated for the purpose of assessing the validity of the assay described in Example 2. Virus stability upon PRRSV replication *in vivo* was studied in four individual gilts, in penmates, and in gilt-piglet relationships. The results are shown in Table III, below. In each of evaluations Nos. 1-3, the virus was passaged *in vivo* in a gilt for a period of 7 weeks. After this time, virus was isolated from a sample taken by lung lavage wherein the alveolar macrophages, which are believed to be the primary cells for virus replication *in vivo*, are flushed from the lung.

In each case, the recovered strain was characterized by the same RE pattern as the exposure strain (RespPRRS®). In evaluation No. 4, the same results were obtained for strain

NADC-8. In evaluation Nos. 5 and 6, a pig was exposed to strain NADC-8, and 8 weeks later brought into contact with a second pig which thereafter shared the same pen. After 3 weeks, the RE pattern of the strain recovered from the second pig was identical to that of Strain NADC-8 used to infect the first pig.

In evaluation No. 7, a pregnant gilt was infected with strain RespPRRS® eight weeks prior to farrowing. The RE pattern of the PPRSV recovered 5 weeks later from one of her piglets was the same as the original strain RespPRRS®.

It is understood that the foregoing detailed description is given merely by way of illustration and that modifications and variations may be made therein without departing from the spirit and scope of the invention.

TABLE I
Restriction Enzyme Analysis of PRRSV Isolates

<u>Strains</u>	<u>ID</u>	<u>Origin</u>	<u>Year</u>	<u>Restricted Enzyme^a</u>			
				<i>Mlu</i> I	<i>Sfc</i> I	<i>Hinc</i> II	<i>Sac</i> II
1	46448	IA	1989	-	-	219	24
2	46907	KY	1991	-	-	-	24
3	1205-D	MO	1992	-	-	-	24
4	10654	IA	1992	-	-	360	-
5	30093-A	IL	1992	-	-	219	24
6	34075	NE	1992	-	-	88,219	24
7	49138	TX	1992	-	-	88,219	24
8	5556	MI	1993	-	-	-	24,555
9	22805	KS	1992	-	-	260	555
10	5591	NC	1993	-	-	219	24
11	14622	AR	1993	-	-	88	24,555
12	19950-E	MN	1993	-	-	88,219	24
13	26948-2	VA	1993	-	-	88	24,555
14	41572-2	NE	1993	-	-	88,219	24,555
15	42928	IL	1993	-	-	88,219	24
16	32983-LG	NC	1993	-	-	88,219	24
17	30352-3	MI	1993	-	-	-	24,555
18	47324-2	CANADA	1993	-	-	88	24,555
19	18310-A	PA	1994	-	-	88	24
20	24901	GUATEMALA	1994	-	-	88,219	24
NADC-8	(IA)-92	IA	1992	-	-	219	24,555
NADC-9	(IA)-93	IA	1993	-	-	219	24,555
RespPRRS®	-	MN ^b		408	116	360	24
VR 2332	-	MN		408	116	360	24

^a The designated cut sides are for the 603 bp ORF 5

^b presumed to originate from strain VR 2332

Table II (A)

ENZYME	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12
AccI	318	318	318	318	318	318	318	318	318	318	318	318
AhaII	xxx	268	268	118	xxx							
AhiI	mult(4)	mult(4)	mult(4)	mult(4)	mult(5)	136/176	136/176	136/176	136/176	136/176	136/176	136/176
ApaLI	xxx											
Apal	192/24	xxx	204	xxx	140/204	204	204	204	204	204	204	204
BaiI	xx	309	309	309	309	309	309	309	309	309	309	309
BanI	267	267	267	267	267	267	267	267	267	267	267	267
BbvI	145/268	145/268	145/268	145/268	145/268	145/268	145/268	145/268	145/268	145/268	145/268	145/268
BglI	192/199	195	195/195	195/195	195/195	195/195	195/195	195/195	195/195	195/195	195/195	195/195
BsuMI	xxx	268	268	118	xxx							
BspAI	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580	493/6580
BstEII	498	498	498	498	498	498	498	498	498	498	498	498
BstI	xxx											
BsmAI	263	263	263	263	263	263	263	263	263	263	263	263
Bsp126I	212/317	317	317	112/272/317	212/317	112/272/317	112/272/317	212/317	112/272/317	112/272/317	112/272/317	112/272/317
BstFII	xxx	324	324	xxx	xxx	324	xxx	xxx	xxx	xxx	xxx	xxx
BaiI	216	xxx	xxx	xxx	xxx	216	xxx	195	195	195	195	195
BstEII	xxx											
BstNI	318/428	318/428	318/428	318/428	318/428	318/428	318/428	318/428	318/428	318/428	318/428	318/428
BstU	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268	5/165/268
Cfr10I	xxx	324	324	xxx	xxx	324	xxx	xxx	xxx	xxx	xxx	xxx
ClaI	xxx											
DdeI	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678	351/472/678
DpnI	549	549	549	549	549	549	549	549	549	549	549	549
DpnII	647	xxx	547	547	547	547	547	547	547	547	547	547
EcoI	xxx	307	307	xxx	xxx	583	xxx	307	xxx	307	xxx	xxx
EcoI	510	xxx	xxx	xxx	610	510	xxx	xxx	510	xxx	xxx	xxx
Eco47III	xxx											
EcoBII	xxx											
Fnu4H	134/382	134/382	134/382	134/382	134/382	134/382	134/382	134/382	134/382	134/382	134/382	134/382
FokI	xxx											
HaeII	12/434	12/127/1434	434	12/127/1434	434	434	434	434	434	434	434	434
HaeIII	xxx	309	309	xxx	309	541	309	xxx	309	309	309	309
HgaI	173	173	173	126/173	173	173	173	173	173	173	173	173
HgaII	xxx	xxx	xxx	112	xxx	112/23/2377	112/23/2377	112/23/2377	112/23/2377	112/23/2377	112/23/2377	112/23/2377
HincII	247	xxx	368	247	116/247	116/247	116/247	116/247	116/247	116/247	116/247	116/247
HinfI	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481

Table II (B)

ENZYME	813	814	815	816	817	818	819	820	NADP-2	NADP-3	REF.7332
Ace I	318	xx	xx	xx	318	318	318	xx	xx	xx	318
Ala B	xx										
Alu I	136/176	136/176	136/176	136/176	136/176	136/176	136/176	136/176	mult(4)	mult(4)	mult(4)
Apa I	268	268	268	268	268	268	268	268	xx	xx	xx
Arg I	204	204	204	204	204	204	204	204	140/204/601	140/204/601	204
Bal I	xx										
Ban I	xx										
Bbv I	mult(4)	mult(4)	145/348	mult(7)	145/348	145/348	145/348	mult(4)	145/348	145/348	145/348
Bgl I	465/679	280/679	629	280/453/229	xx	280	629	629	195/289	195/289	195
Bsa HI	xx										
Bse XI	493/765/90	mult(4)	493/765/90	493/765/90	493/50	mult(4)	493/50	493/50	493/765/90	493/765/90	493/765/90
Bsi EI	498	498	498	498	xx	498	498	xx	498	498	498
Bst I	xx										
Bam AI	xx										
Bbv 1235I	1122/22/317	1122/22/317	1122/22/317	1122/22/317	272/3/77	1122/22/317	1122/22/317	1122/22/317	272/3/77	272/3/77	1122/22/317
Bbv F1	xx	324	324	xx							
Bgl I	xx										
Bst EII	206	549	xx	xx	xx	xx	xx	xx	216	216	xx
Bst N	378/428	380/428	380/428	378/428	378/428	378/428	378/428	378/428	378/428	378/428	378/428
Bst U	mult(4)	mult(4)	51/65/368	61/65/368	mult(4)	mult(4)	51/65	51/65/368	51/368/532	51/368/532	mult(4)
Cla I	xx										
Dra I	xx										
Dra I	351/472	351/472	472	351/472/352	351/472/352	472	472	472	351/472/218	351/472/218	351/472/218
Dra I	549	549	497/549	549	549	549	549	549	549	549	549
Dra II	547	547	495/547	547	547	547	547	547	547	547	547
Eco I	xx										
Eco I	xx										
Eco 47II	xx										
Eco R I	xx										
Eco 47II	mult(5)	mult(5)	134/347	mult(7)	134/347/53	134/347/53	mult(4)	134/347/53	134/347/53	134/347/53	134/347/53
Fok I	xx										
Hae II	434	434	130/434	434	121/434	434	434	434	121/434	121/434	434
Hae III	xx										
Hha I	173	173	173	173	173	173	173	173	173	173	173
Hha II	112/212	112/212	112/212	112/212	xx	112	112/212/217	112/212/217	xx	xx	112
Hha I	433	433	128/433	433	110/120/433	375/433	433	433	110/120/433	433	433
Hinc II	116	116	116/247	116/247	xx	116	116	116	116/247	247	247
Hinf I	491	248/491	248/491	248/491	248/491	248/491	248/491	248/491	248/491	248/491	248/491

Table II (C)

ENZYME	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12
Hind I	1089/18431	mutil(4)	431	1089/18431	431	1089/18431	431	1089/18431	431	431	431	431
Hpa II	325	325	325	325	325	325	325	325	325	325	325	325
Hph I	325	325	325	325	325	325	325	325	325	325	325	325
Kis I	325	325	325	325	325	325	325	325	325	325	325	325
Kas I	195/289	195/199	195	195/445	195/250/318	308/455/6279	455/619	195/192/626	195/145	629	629	629
Kpn II	325	325	325	325	325	325	325	325	325	325	325	325
Mbo I	547	547	547	547	547	547	547	547	547	547	547	547
Mbo II	425/453/527	324/425/453	324/425/453	425/453/527	425/453/527	324/425/453	425	227/453	425	425/453	425	425
Msp I	325	325	325	325	325	325	325	325	325	325	325	325
Mnl I	mutil(4)	282/523/584	282/523/584	282/523/584	mutil(4)	523/584	471/523/584	282/523/584	282/523/584	523/584	523/584	523/584
Msp I	325	325	325	325	325	325	325	325	325	325	325	325
Nla I	325	325	325	325	325	325	325	325	325	325	325	325
Nla III	425/442	323/442	323/442	425/442	425/442	425/442	425/442	425/320/442	425/442	425	425	425
Nla IV	282/578	282/578	282/578	282/578	282/578	282/578	282/578	282/578	282/578	282/578	282/578	282/578
Nru I	325	325	325	325	325	325	325	325	325	325	325	325
Nsp BI	51/149	51/149/629	51/149/629	509	51/149	51/149	51	51/52/629	52/629	51/629	51/629	51/629
Nsp HI	425	425	425	425	425	425	425	425	425	425	425	425
Pst I	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475
Pst II	425	425	425	425	425	425	425	425	425	425	425	425
Rsa I	443	443	443	443	443	443	443	443	443	443	443	443
Sac II	52	52	52	52	52	52	52	52	52	52	52	52
Sph III	547	547	547	547	547	547	547	547	547	547	547	547
Sph I	325	325	325	325	325	325	325	325	325	325	325	325
Sst I	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428	326/378/428
Sst I	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80	493/785/80
Sst N	387	387	387	387	387	387	387	387	387	387	387	387
Sst I	325	325	325	325	325	325	325	325	325	325	325	325
Sst I	325	325	325	325	325	325	325	325	325	325	325	325
Taq I	535/550	535/550	535/550	535/550	535/550	535/550	535/550	535/550	535/550	535/550	535/550	535/550
Tth I	297	297	297	297	297	297	297	297	297	297	297	297
Xba I	461	461	461	461	461	461	461	461	461	461	461	461
Xcm I	-	-	-	-	-	-	-	-	-	-	-	-

Table II (D)

ENZYME	\$13	\$14	\$15	\$16	\$17	\$18	\$19	\$20	NADC-9	NADC-8	NADC-9	REF-Y332
Hind P	431	127431	491	108418431	372431	431	431	108418431	108418431	108418431	431	
Hpa II	325609	325	325	325	325	325	325	325	325	325	325	
Hph I	590	534	668	303	47690	100	266534	47668534	534	534	534	
Kpn I	300	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Mae I	4656729	2806729	629	202465321	303	280	829	879	185280	185280	185280	195
Mae III	308	308540	308	308	496	308	308540	308540	308540	308540	308540	
Msp I	547	495547	—	547	—	547	—	547	—	547	—	
Mbo II	324475	423	423	423	4254153	3244254153	425	425	425453	425453	425453	453
Msp II	353	353	353	353	353	353	353	353	353	353	353	
Msp I	333573564	523564	523564	523564	282523564	523564	523564	486523564	282523564	282523564	282523564	
Msp I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Msp I	594	387594	586	387594	xx	xx	594	594	xx	xx	xx	
Msp I	375689	373	373	373	325	375	xx	375	375	375	375	
Msp I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Nar I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Nci I	376	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Nhe I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Nla III	425442	425442	425442	425442	425442	425442	425	425	425442	425442	425442	475
Nla IV	578	578	578	578	269578	269578	578	578	269578	269578	269578	
Nru I	65	65	65	65	65	65	65	65	xx	xx	xx	65
Nru II	51552	515520509	5155209	5155209	5155209	5155209	multif(4)	5155209	multif(4)	5155209	5155209	
Nsp II	425	425	425	425	425	425	425	425	425	425	425	
Pst I	475	242475	242475	242475	242475	242475	242475	242475	242475	242475	242475	
Pvu I	xx	xx	488	xx	xx	xx	xx	xx	xx	xx	xx	
Pvu II	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Rsa I	185	443	443	443	443	443	443	443	443	443	443	443
Sac II	52559	52559	57	52	52553	52553	52	52	52553	52553	52553	52
Sac III	547	495547	547	547	xx	xx	547	547	547	547	547	
Sau 36I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Sce F	326376426	378426	843276426	326376426	378426	326376426	378426	326376426	326376426	326376426	326376426	
Sce I	49378550	multif(4)	49378550	49378550	49378550	49378550	49378550	49378550	49378550	49378550	49378550	
Sfa NI	367	367	367	367	367	367	367	367	367	367	367	
Sfc I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Sfi I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Sly I	472	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Tag I	535550	535550	535550	535550	535550	535550	535550	535550	535550	535550	535550	
Tth 111I	297	297	297	297	xx	xx	xx	xx	xx	xx	xx	
Xba I	484	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	
Xcm I	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	xx	

TABLE III

Restriction Enzyme Pattern after PRRSV Replication in vivo

No.	Type	Sample	Source	Duration of		PRRSV Strain	Recovered
				Infection	Exposure		
1	Lung-Lavage	Gilt		7 wks		Respprrs®	
2	"	"		"	"	"	"
3	"	"		"	"	"	"
4	"	"		"		NADC-8	
5	Pig-Pig			8 + 3			
6	"	"		8 + 3	"	"	"
7	Gilt-Piglet			8 + 5		Respprrs®	Respprrs®

REFERENCES

Balasuriya UBR, MacLachan NJ, DeVries AAF, Rossitto PV, Rottier PJM (1995) Identification of a neutralization site in the major envelope glycoprotein (G_t) of equine arteritis virus. *Virology* 207:518-527.

Bautista EM, Goyal SM, Collins JE (1993) Serologic survey for Lelystad and VR-2332 strains of porcine respiratory and reproductive syndrome (PRRS) virus in US swine herds. *J Vet Diagn Invest* 5:621-614.

Conzelmann KK, Visser N, Van Woensel P, Thiel HJ (1993) Molecular characterization of porcine reproductive and respiratory syndrome virus, a member of the Arteritis group. *Virology* 193:329-339.

De Vries AAF, Chirnside ED, Horzinek MC, Rottier PJM (1992) Structural proteins of equine arteritis virus. *J Virol* 6:6294-6303.

Godeny EK, Chen L, Kumar SN, Methven SL, Koonin EV, Brinton MA (1993) Complete genomic sequence and phylogenetic analysis of the lactate dehydrogenase-elevating virus (LDV). *Virology* 194:585-596.

Harty JT and Plagemann PGW (1988) Formalin inactivation of the lactate dehydrogenase-elevating virus reveals a major neutralizing epitope not recognized during natural infection. *J of Virol* 62:3210-3216.

Keffaber, K.K., (1989) Reproducing failure of unknown etiology.
Am. Assoc. Swine Pract. News 1:1-10.

Kim HS, Kwang J, Yoon IJ, Joo HS, Frey ML (1993) Enhanced replication of porcine reproductive and respiratory syndrome (PRRS) virus in a homogeneous subpopulation of MA-104 cell line. Arch Virol 133:477-483.

Loula, T. (1991) Mystery pig disease. Agri. Pract. 12:23-33.

Meng XJ, Paul PS, Halbur PG, (1994) Molecular cloning and nucleotide sequencing of the 3'-terminal genomic RNA of the porcine reproductive and respiratory syndrome virus. J of Gen Virol 75:1795-1801.

Meng XJ, Paul PS, Halbur PG, Lum MA (1995) Phylogenetic analyses of the putative M (ORF 6) and N (ORF 7) genes of porcine reproductive and respiratory syndrome virus (PRRSV): implication for the existence of two genotypes of PRRSV in the U.S.A. and Europe. Arch Virol 140:745-755.

Meulenberg JJM, Hulst MM, De Meijer EJ, Moonen PLJM, Den Besten A, De Kluyver EP, Wensvoort G, Moormann RJM (1993) Lelystad virus, the causative agent of porcine epidemic abortion and respiratory syndrome (PEARS), is related to LVD and EAV. Virology 192:62-72.

Meulenberg JJM, Petersen-Den Besten A, De Kluyver EP, Moormann RJM, Schaaper WMM, Wensvoort G (1995) Characterization of proteins encoded by ORFs 2 to 7 of Lelystad virus. Virology 206:155-163.

Morozov I, Meng XJ, Paul PS (1995) Sequence analysis of open reading frames (ORFs) 2 to 4 of a U.S. Isolate of porcine reproductive and respiratory syndrome virus. *Arch Virol* 140:1313-1319.

Persch S, Heinen E, Schmeer N, Ohlinger VF (1995) Antigenic variations between different PRRSV-isolates. In Proceedings of the Second International Symposium on Porcine Reproductive and Respiratory Syndrome (PRRS), Copenhagen, Denmark p. 7.

Plagemann PG and Moenning V (1992) Lactate dehydrogenase-elevating virus, equine arteritis virus and simian hemorrhagic fever virus, a new group of positive strand RNA virus. *Advances in Virus Research* 41:99-192.

Sambrook J, Fritsch EF, Maniatis T (1989) Molecular Cloning; A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Springs Harbor, N.Y., 2nd ed.

Sanger F, Nicklen S, Coulson AR (1977) DNA sequencing with chain terminating inhibitors. *Proc Natl Acad Sci U.S.A.* 74:5463-5464.

Sellner LN, Coelen RJ, Mackenzie JS (1992) A one-tube, one manipulation RT-PCR reaction for detection of Ross River virus. *J. Virol. Meth.*, 40:255-264 Snijder EJ and Spaan WJM (1995).

Snijder EJ and Spaan WJM (1995) The Coronaviruslike Superfamily. In The Coronaviridae. Ed. Siddell SG. New York: Plenum Press.

Tabor S and Richardson CC (1987) DNA sequence analysis with a modified bacteriophage T7DNA polymerase. *Proc Natl Acad Sci U.S.A.* 84:4767-4771.

Van Nieuwstadt A, Meulenberg J., Van Essen-Zandbergen A, Petersen-Den Besten A, Bende R, Moormann R, Wensvoort G (1995) Monoclonal antibodies specific for lelystad virus recognize two additional structural viral proteins, encoded by ORF3 and ORF4 of the viral genome. In *Proceedings of the Second International Symposium on Porcine Reproductive and Respiratory Syndrome Virus (PRRS)*, Copenhagen, Denmark, p. 5.

Wensvoort G, Terpstra C, Pol JMA, ter Laak EA, Bloemraad M, de Kluyver EP, Kragten C, Van Buiten KL, den Besten A, Wagenaar F, Broekhuijsen JM, Moonen PLJM, Zetsstra T, de Boer EA, Tibben HJ, de Jong MF, van't Veld P, Groenland GJR, van Gennep JA, Voets MT, Verheijden JHM, Braamkamp J (1991) Mystery swine disease in the Netherlands: the isolation of Lelystad virus. *Vet. Q.* 13:121-130.

Wensvoort G, de Kluyver EP, Luijze EA, den Besten A, Harris L, Collins JE, Christianson WT, Chladek D (1992) Antigenic comparison of Lelystad virus and swine infertility and respiratory syndrome (SIRS) virus. *J of Vet Diag Invest* 4:134-138.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: The United States of America, as
Represented by the Secretary of
Agriculture

(ii) TITLE OF INVENTION: Restriction Enzyme Screen for
Differentiating Porcine Reproductive and Respiratory
Syndrome Virus Strains

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

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- (B) STREET: 1815 N. University Street
- (C) CITY: Peoria
- (D) STATE: IL
- (E) COUNTRY: USA
- (F) ZIP: 61604

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Ribando, Curtis P.
- (B) REGISTRATION NUMBER: 27,976

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 309-681-6513
- (B) TELEFAX: 309-681-6688

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 46448 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGTTGGGTA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTG GTGGTGTATC	60
GTGCCGTCTT GTTTGTTCGC GCTCGTCAGC GCCAACGGGA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAAATT	180
GACTGGGCAG TGGAGTGTCTT TGTCACTTTT CCCGTGTGA CTCACATTGT CTCTTATGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TCACTGTGTC TACCGCCGGG	300
TTTGTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGGGG TCTGTGCCCT GGCTGGTGTG	360
ATTTGCTTCG TCATTAGGTT TCGGAAGAAT TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATAACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAGA GGGGTAAAGT TGAGGTCGAA GGTCACTGTA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AAAGTTTCAG CAGAACAAATG GGGTCGTCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 46907 (KY)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTG GTGGTGTATC	60
GTGCCGTCCT GTTTTGTTGC GCTCGTCAGC GCCAACAGCA ACAGCAGCTC CCATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAGTAGATT	180
GATTGGGCAG TGGAGTGTTT TGTCATCTTT CCTGTGCTGA CTCACATTGT CTCCTATGGC	240
GCCCTCACTA CCAGCCATTG CCTTGACACA GTCGGTCTGG CCACTGTGTC TACCGCCGGT	300
TTCCTTCGCG GGCGGTATGT TCTGAGTAGC ATCTACGGG TCTGTGCCCT GGCTGCGTTG	360
TTTGCTTCG TCATTAGATT GGCGAAGAAT TGCATGTCCT GGCGCTATTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA TACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAA AGGGTAAAGT TGAGGTCGAA GGTCACTCTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTGTAACC AGAGTTTCAG CGGAACAAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 1205-D(MO)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTT GTGGTGTATC	60
GTGCCGTCCT GTTTGTGTC GCTCGTCAGC GCCAACAGCA ACAGCAGCTC TCATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATT	180
GATTGGGCAG TCGGAATGTTT TGTCACTCTT CCTGTGCTGA CTCACATTGT CTCCTATGGC	240
GCCCTCACTA CCAGCCATT CCTTGACACA TTCTGGCTGG CCACTGTGTC TACCGCCGGT	300
TTTCTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCCGTTG	360
TTTTGCTTCG TCATTAAGATT TGGAAAGAAT TGCATGTCCT GGCGCTATTG ATGTACCAGA	420
TATACCAACT TTCTTCCTGGA TACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAA AGGGTAAAGT TGAGGTCGAA GGTCACTGAA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTGTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 10654 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTT GTGGTGTATC	60
GTGCCGTCTT GTCTTGTTC GCTCGTCAGC GCCAACGGGA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATT	180
GACTGGGCAG TGGAGTGT TT TGTCATTTT CCCGTGTTGA CTCACATTGT CTCTTACGGT	240
GCCCTCACTA CTAGCCATT CCTTGACACA GTCGGCCTGG TCACTGTGTC TACCGCCGGG	300
TTTGTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT AGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGCGAAGAAAT TGCAATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACTAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAGA GGGGTAAAGT TGAGGTCGAA GGTCACTGTA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CAGAACATG GGGTCGTCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 30093-A(IL)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTT GTGGTGTATC	60
GTGCCGTCTT GTCTTGTTC GCTCGTCAGC GCCAACGGGA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATT	180
GACTGGGCAG TGGAGTGTGT TGTCACTTTT CCCGTGTTGA CTCACATTGT CTCTTACGGT	240
GCCCTCACTA CTAGCCATT CCTTGACACA GTCGGCCTGG TCACTGTGTC TACCGCCGGG	300
TTTGTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT AGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGCGAAGAAT TGCAATGTCTT GGCCTACTC ATGTACCAGA	420
TATACTAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAGA GGGGTAAAGT TGAGGTCGAA GGTCAATCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CAGAACAAATG GGGTCGTCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 34075 (NE)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTTGCGAT TGCTTCTTT GTGGTGTATC	60
GTGCCGTTCT TTTTGCTGT GCTCGTCAAC GCCAACAGCA CCAGCAGCTC CCATTTGCAG	120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TAATAAATT	180
GATTGGGCAG TGGAGAGTTT TGTTATTTTT CCCGTGTTGA CTCACATTGT TTCCATGGT	240
GCACTCACCA CCAGCCATTT CCTTGACACA GTCGGTCTAG TTACTGTGTC CACCGCCGGT	300
TTCTTCACG GGCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
GTTTGCTTCG GCATTAGGTT TGCGAAGAAC TGCATGTCCCT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTAGA CACCAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGTAAGGT TGAGGTCGCA GGTACCTAA TCGACCTCCA AAGAGTTGTG	540
CCTGATGGTT CCGTGGCCAC TCCTTTAACCC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 49138 (TX)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA ACAGCAGCTC TCATTTTCAG	120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ACTGGCTGGC TAACAAATT	180
GATTGGGCAG TGGAGACTTT TGTCACTCTT CCCGTGTTGA CTCACATTGT TTCTATGGT	240
GCACTCACCA CCAGCCATT CCTTGACACA GTTGGCTGGG TTACTGTGTC CACCGCCGGG	300
TTTTATCACG GGCGGTATGT CTTGAGTAGC ATCTACGCCG TCTGTGCTCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGCGAAGAAC TGCGATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TCCTCCTAGA TACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGCCACCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC TCCTTTAACCC AGAGTTTCAG CAGAACATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 5556 (MI)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGTTGGTGA GATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTG GTGGTGTATC	60
GTGCCGTCTT GTTTTGTTCG GCTCGTCAGC GCCAACATAA GCAGCAGCTC TCATTACACAG	120
TTGATTTACA ACCTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAGTAAATTT	180
GATTGGGCAG TGGAGTGGCTT TGTCATCTTC CCTGTGGCTGA CTCACATTGT CTCCTATGGT	240
GCCCTCACTA CCAGCCATTG TCTTGACACA GTCGGTCTGG CCACTGTGTC TACCGCCGGG	300
TTCGTTCACTG GGCGGTATGT TCTGAGTAGC ATCTACGGGG TCTGTGCCCT GGCTGGTGTG	360
ATTTGCTTCG TCATCAGGTT TGTGAAAAAT TGCATGTCAT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC ACCTGTCATC	480
ATAGAGAAAA AGGGTAAAGT TGAGGTCGAA GGTCACTGAA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CGCGGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCATCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 22805 (KS)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGTTGGGGA AATGCTTGAC CGTGGGCTGT TGCTCGCGAT TGCCTTCITT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTGCCAAC GCTCACGGCA ACAGCAGCTC TCATCTGCAA	120
TTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TGATAGATT	180
GATTGGGCAG TGGAGAGCTT TGTCACTTT CCTGTTTGA CTCACATTGT CTCCATGGT	240
GCCCTCACTA CCAGCCATTG CCTTGACACA ATTGCTTAG TCACGTGTC TACCGCCGGG	300
TTTGTTCACA GGCGGTATGT CCTGAGTAGC ATCTACGCAG TCTGTGCCCT GGCTGCGTTG	360
ACTTGCTTCG TCATTAAGGTT TGAAAGAAT TGCATGTCCT GGCGCTACTC ATGTACTAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAGA GGGGCAAGGT TGAGGTCGAA GGTCATCTGA TTGATCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 5591(NC)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGTTGGGGA AATGCTTGAC CGCGGATTGT TGCTCGCGAT TGCTTTTTT GTGGTGTATC	60
GTGCCGTTCT GGTTTGCTGT GCTCGGCAAC GCCAACAGCA CCAGCAGCTC TCACTTACAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGTTGGC TAACAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTTATTTTT CCCGTGTTGA CTCACATTGT TTCCATGGT	240
GCACTCACCA CCAGCCATTTC CCTTGACACA GTCGGTCTGG TTACTGTGTC TACCGCCGGG	300
TTTTGTCACG GGCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCTCT GGCCCGCTTG	360
ATTTGTTTCG TCATCAGGTT TGCGAAGAAC TGCATGTCTT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGATC GCCTGTCATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGCCATCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACCG AGAGTTTCAG CGGAACAATG GGGTCGTCCC.	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 14622 (AR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTCTTT GTGGTTTATC	60
GTGCCGTTCT GTTTTGTGT GCTCGTCAAC GCCAACAGCA ACAGCAGCTC TCATTACAG	120
TTGATTATA ACCTGACGCT ATGTGAGCTG <u>AATGGCACAG ATTGGCTGGC TAATAAAATT</u>	180
GATTGGGCAG TGGAGAGTTT TGTCACTTT CCTGTGCTGA CTCACATTGT CTCTTATAGT	240
GCCCTCACTA CCAGCCATTTC CCTTGACACA GTCGGTCTGG CCACTGTGTC TACCGCCGGA	300
TTTGTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGCGCCCT GGCTGCGTTG	360
ATTTGTTCA TCATCAGGTT TGCGAAGAAAT TGCAATGTCTT GGCGCTACTC TTGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCATCTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTGTAACC AAAGTTTCAG CGGAACAATG GGGTCATCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 19950-E (MN)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGAGAAATTT	180
GATTGGGCGG TGGAAAGTTT TGTCACTTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACTA CTAGCCATTT TCTTGACACA GTCGGTCTGG TTACTGTGTC TACCGCCGGG	300
TTTTGGCACG GGCGGTATGT CTTGAGCAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTA	360
ATTTGCTTGT TCATTAGGCT TGCGAAGAAC TGCAATGTCCT GGCGCTACTC TTGTACCAGA	420
TATACTAACT TCCTTCTAGA CACTAAGGGC AGACTCTATC GTTGGGGTC GCCCGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGTCACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACCC AGAGTTTCAG CGGAACAAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 26948-2 (VA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCCTTTTT GTGGTGTATC	60
GTGCCGTTCT GTTTGGTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGTACAG ATTGGCTGGC AGGAAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTCACTTTT CCCGTGCTGA CCCACATTGT TTCCATATGGT	240
GCACCTACTA CCAGCCATTT CCTTGACACA GTCGGTCTGG TTACCGTGTC TACCGCCGGG	300
TTTCTTCACG GGAGGTATGT CCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGCT TCGAAAGAAC TGCATGTCCCT GGCCTACTC ATGCACCAGA	420
TATACCAACT TCCTTCTAGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTTATC	480
ATAGAAAAAA AAGGTAAGGT TGAGGTCGAA GGTCACTGAA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC TCCTTTAACCGAGAGTTTCAC CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 41572-2 (NE)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTCTTT GTGGTGTATC	60
GTGCCGTTCT GGTTTGCTGT GCTCGTCAAC GCCAGCAGCA ACAGCAGCTC TCATTTTCAG	120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TAATAAAATT	180
GATTGGGCAG TGGAGAGTTT TGTCACTTT CCTGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TTACTGTGTC CACCGCCGGT	300
TTTTTCACG GGCGGTATGT CTTGAGCAGC ATCTACGGG TCTGTGCCCT GGCTGCGTTA	360
ATTTGCTTTG TCATTAGGCT TGCGAAGAAC TGCAATGTCTT GGCGCTACTC ATGTACCAGA	420
TATACCAACT CCCTTCTGGA CACCAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTTATC	480
ATAGAGAAAA GGGGTAAGGT TGAGGTCGAA GGTACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CGCGGGCTAC CCCTTAACC AGAGTTCTAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 42928 (IL)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTCCT GGTTTGCTGT GCTCGTCAAC GCCAACAGCG CCAGCAGCTC TCATTTGCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGTTGGC TGACAAGTTT	180
GATTGGGCAG TGGAGACTTT TGTCTTTAT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CCTTGACACA GTCGGTCTGG TTACTGTGTC CACCGCCGGT	300
TTTGTTCACG GGCGGTATGT CTTGAGTAGC ATCTACGGGG TCTGTGCCCT GGCTGCGTTG	360
AGTTGTTTTG TCATCAGGTT TGTGAAGAAC TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACCAAAT TCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGATC GCCTGTCATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGCCATCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTAACCC AGAGTTTCAG CGGAACGATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 32983-LG(NC)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGC TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTCGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGGGAATT	180
GATTGGGCGG TGGAAAGTTT TGTCACTTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACACTACA CTAGCCATTT TCTTGACACA GTCGGTCTGG TTACTGTGTC TACCGCCGGG	300
TTTTTGCACTG GGCGGTATGT CTTGAGCAGC ATCTACGCGG TTTGTGCCCT GGCTGCGTTA	360
ATTTGCTTTG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACTAACT CCCTTCTAGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGTCATCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACCC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 30352-3 (MI)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGTTGGTGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTG GTGGTGTATC	60
GTGCCGTCCT GTTTTGTGCG GCTCGTCAGC GCCAACGCCA ACAGCAGCTC CCATTCACAG	120
TTGATTTACA ACCTGACGCT ATGTGAGCTG AATGGCAGCAG ATTGGCTGTC TAATAAAATT	180
GATTGGGCAG TGGAGTGTGTT TGTCACTTT CCTGTGCTGA CTCACATTGT CTCCCTATGGT	240
GCCCTCACTA CCAGCCATTT CCTTGACACA GTCGGTCTGG CCGTTGTGTC TACCGCCGGG	300
TTTGTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT TGCTGCGTTG	360
ATTTGCTTCG TCATTAGATT TGCAGAAGAAT TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC ACCTGTCATC	480
ATAGAGAAAA GGGGTAAAGT TGAGGTCGAA GGTAATCTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CGCGGGCAAC CCCATAACC AAAGTTTCAG CGGAACAATG GGGTCATCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 47324-2 (CAN)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTG GTGGTGTATC	60
GTGCCGTCCT GTTTTGTGT GCTCGTCAAC GCCAACACAA GAAGCAGCTC CCATTTTCAG	120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGATAAAATT	180
GATTGGGCAG TGGAGAGTTT TGTCACTTTT CCCGTTTGA CTCACATTGT TTCCTATGGT	240
GCCCTAACCA CTAGCCATT TCTTGACACA GTTGGTCTGG TTACTGTGTC TACCGCTGGT	300
TTTCTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGGGG TCTGCGCCCT GGCTGCGTTG	360
ATTTGTTTG TCATTAGGTT CGTGAAGAAC TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
CATACCAACT TTCTTCTGGA TACCAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAG GGGGTAAAGT TGAGGTCGAA GGTCATCTCA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAAATG GGGTCGTCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 18310-A(PA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGTGT GCTCGTCAAC GCCAACAGCA ACAGCAGCTC TCATTTTCAG	120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ACTGGCTGGC TAACAAATT	180
GATTGGGCAG TGGAGACTTT TGTCACTTTT CCCGTATTGA CTCACATTGT TTCTATGGT	240
GCACTCACCA CCAGCCATT CTTGACACA GTTGGCTGG TTACTGTGTC CACCGCCGGG	300
TTTTATCAGG GGCGGTATGT CTTGAGTAGC ATCTATGCGG TCTGTGCTCT GGCTGCGTTG	360
TTTGCTTCG TCATTAGGCT TGCGAAGAAC TGCATGTCTT GGCGCTACTC TTGTACCAGA	420
TATACCAACT CCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTTATT	480
ATAGAGAAAG GGGTAAGGT TGAGGTCGAA GGTCACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CGTGGCAAC CCCTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCTC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 24901 (GUA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGTTGGTGA AATGCTTGAC CGCGGGCCGT TGCTCGCGAT TGCCTTTTT GTGGTGTATC	60
GTGCCGTTCT GTTTGCTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGACAAATT	180
GATTTGGGCAG TAGAGACTTT TGTCACTTT CCCGTGTGTA CTCACATTGT TTCTATGGT	240
GCACTCACCA CCAGCCATT CTTGACACA GTTGGTCTGG TTACTGTGTC CACCGCCGGG	300
TTTTATCACG GGCGGTATGT CTGAGTAGC ATCTACGCGG TCTGTGCTCT GGCTGCGTTG	360
ATTTGCTTCG TCATTTAGGCT TGCGAAGAAC TGCATGTCCT GGCGCTACTC TTGTACCAGA	420
TATACCAACT TCCCTCTGGA CACTAAGGGC AGACTCTATC GTTGGAGGTC GCCCGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGTCACCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: NADC-8 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTT GTGGTGTATC	60
GTCGCCGTCTT GTTTTGTGTC GCTCGTCAGC GCCAACAGCA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATT	180
GACTGGGCAG TGGAGTGTGTT TGTCACTTT CCTGTGTTGA CTCACATTGT CTCTTATGGT	240
GCCCTCACTA CTAGCCATTG CCTTGACACA GTCGGTCTGG TCACTGTGTC CACCGCCGGA	300
TTTTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGGG TCTGTGCCCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGCT TGCGAAGAAT TGCAATGTCTT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CC CGCGGCAAC CCCTGTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: NADC-9 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGTTGGTGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTTG GTGGTGTATC	60
GTGTCGTCTCT GTTTTGTAGC GCTCGTCAGC GCCAACACGA CCAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATT	180
GACTGGGCAG TGGAGTGTGGT TTGTCATTTT CCTGTGTTGA CTCACATTGT CTCTTATGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TCACTGTGTC CACCGCCGGG	300
TTTGTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGGGG TCTGTGCCCT GGCTGGCTTG	360
ATTTGCTTCG TCATTAGGCT TGCAGAAAC TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACCAAAT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
GTAGAGAAAA GGGGCAAGGT CGAGGTCGAA GGTCACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CGCGGGCAAC TCCTGTAACC AGAATTTCAT CAGAACAAATG GGGTCGTCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: RespPRRS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCCAGCAACG ACAGCAGCTC CCATCTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAACAAATT	180
GATTGGGCAG TGGAGAGTTT TGTCATCTTT CCCGTTTGA CTCACATTGT CTCCATATGGT	240
GCCCTCACTA CCAGCCATTG CCTTGACACA GTCGCTTAG TCACGTGTC TACCGCCGGG	300
TTTGTTCACG GGCGGTATGT CCTAAGTAGGC ATCTACGGG TCTGTGCCCT GGCTGCGTTG	360
ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCCT GGCGCTACGC GTGTACCAGA	420
TATAACCAACT TTCTTCTGGA CACTAAGGGC GGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCATCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 2332 (MN)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCCAGCAACG ACAGCAGCTC CCATCTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAACAAATT	180
GATTGGGCAG TGGAGAGTTT TGTCACTTT CCCGTTTGA CTCACATTGT CTCCTATGGT	240
GCCCTCACTA CCAGCCATT CTTGACACA GTCGCTTTAG TCACTGTGTC TACCGCCGGG	300
TTTGTTCACG GGCGGTATGT CCTAAGTAGC ATCTACGGG TCTGTGCCCT GGCTGCGTTG	360
ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCTT GGCGCTACGC GTGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCATCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAAATG GGGTCGTCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCATTCTGTT GGCAATTGGA

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCATATATC ATCACTGGCG

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: RespPRRS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCATTCTGTT GGCAATTGAG ATGTTAACGT ATGTTGGAGA AATGCTTGAC CGCGGGCTGT	60
TGCTCGCAAT TGCTTTCCTTT GTGGGTATC GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC	120
GCCAGCAACG ACAGCAGCTC CCATCTACAG CTGATTTACA ACTTGACGCT ATGTGAGCTG	180
AATGGCACAG ATTGGCTAGC TAACAAATTT GATTGGGCAG TGGAGAGTTT TGTCATCTTT	240
CCCGTTTGA CTCACATTGT CTCCTATGGT GCCCTCACTA CCAGCCATTT CCTTGACACCA	300
GTGGCTTAG TCACTGTGTC TACCGCCGGG TTTGTTCACG GGCGGTATGT CCTAAGTAGC	360
ATCTACGCGG TCTGTGCCCT GGCTGCGTTG ACTTGCTTCG TCATTAGGTT TGCAAAGAAT	420
TGCATGTCCT GGCCTACGC GTGTACCAAGA TATACCAACT TTCTTCTGGA CACTAAGGGC	480
GGACTCTATC GTTGGCGGTC GCCTGTCATC ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA	540
GGTCATCTGA TCGACCTCAA AAGAGTTGTG CTTGATGGTT CCGTGGCAAC CCCTATAACC	600
AGAGTTTCAG CGGAACAATG GGGTCGTCCCT TAGATGACTT CTGTCATGAT AGCACGGCTC	660
CAGAAAAGGT GCTTTGGCG TTTTCTATTA CCTACACGCC AGTGATGATA TATGCC	716

We Claim:

1. A method for differentiating a first strain of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from a second strain of said virus comprising the steps:
 - a. selecting at least one restriction enzyme which yields a distinctive fragment profile from ORF 5 cDNA from each of said first and second strains;
 - b. cleaving the ORF 5 cDNA of said first and second strains with said at least one restriction enzyme;
 - c. comparing the restriction enzyme fragment patterns resulting from step (b).
2. The method as described in Claim 1 wherein one of said strains is the vaccine strain RespPRRS® of PRRSV.
3. The method as described in Claim 2 wherein said restriction enzyme is selected from the group consisting of *Mlu I* and *Sfc I*.
4. The method as described in Claim 1 wherein said restriction enzyme is selected from the group consisting of *Mlu I*, *Sfc I*, *Hinc II* and *Sac II*.
5. A kit for differentiating a first strain of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from a second strain of said virus comprising a pair of primers for amplifying ORF 5 cDNA from each of said first and second strains and at least one restriction enzyme which yields a distinctive fragment profile for the ORF 5 cDNA from each of said first and second strains.

6. The kit of Claim 5 wherein said restriction enzyme is selected from the group consisting of *Mlu* I and *Sfc* I.

7. The kit of Claim 5 wherein said restriction enzyme is selected from the group consisting of *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II.

8. The kit of Claim 5 wherein said primers have the sequence of SEQ ID NO:25 and SEQ ID NO:26.

RespPRRS	ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCCGAT TCCTTTCCTT	50
VR 2332	ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCCGAT TCCTTTCCTT	50
Consensus	ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCCGAT TCCTTTCCTT	50
RespPRRS	CTGGTGTATC GTGCCGTTCT CTGGTGTATC GCTCCCCAAC GCCAGCAACG	100
VR 2332	CTGGTGTATC GTGCCGTTCT CTGGTGTATC GCTCCCCAAC GCCAGCAACG	100
Consensus	CTGGTGTATC GTGCCGTTCT CTGGTGTATC GCTCCCCAAC GCCAGCAACG	100
RespPRRS	ACAGCAGCTC CCATCTACAG CTGATTTACA ACTTGAGCCT ATGTGAGCTG	150
VR 2332	ACAGCAGCTC CCATCTACAG CTGATTTACA ACTTGAGCCT ATGTGAGCTG	150
Consensus	ACAGCAGCTC CCATCTACAG CTGATTTACA ACTTGAGCCT ATGTGAGCTG	150
RespPRRS	AATGGCACAG ATTGGCTAGC TAACAAATTG GATTGGCCAG TGGAGAGTTT	200
VR 2332	AATGGCACAG ATTGGCTAGC TAACAAATTG GATTGGCCAG TGGAGAGTTT	200
Consensus	AATGGCACAG ATTGGCTAGC TAACAAATTG GATTGGCCAG TGGAGAGTTT	200
RespPRRS	TGTCATCTTT CCCGTTTGA CTCACATTTG CTCTTATGGT GCCCTCACTA	250
VR 2332	TGTCATCTTT CCCGTTTGA CTCACATTTG CTCTTATGGT GCCCTCACTA	250
Consensus	TGTCATCTTT CCCGTTTGA CTCACATTTG CTCTTATGGT GCCCTCACTA	250
RespPRRS	CCAGCCATTT CCTTGACACA GTGCCCTTAG TCACTGTGTC TACGGGGGGG	300
VR 2332	CCAGCCATTT CCTTGACACA GTGCCCTTAG TCACTGTGTC TACGGGGGGG	300
Consensus	CCAGCCATTT CCTTGACACA GTGCCCTTAG TCACTGTGTC TACGGGGGGG	300
RespPRRS	TTTGTTCACG GGCGGTATGT CCTAAGTAGC ATCTACGGGG TCTGTGCCCT	350
VR 2332	TTTGTTCACG GGCGGTATGT CCTAAGTAGC ATCTACGGGG TCTGTGCCCT	350
Consensus	TTTGTTCACG GGCGGTATGT CCTAAGTAGC ATCTACGGGG TCTGTGCCCT	350
RespPRRS	CCCTGGTTG ACTTGCTTCG TCATTAGTT TGCAAAGAAT TGCAATGTCC	400
VR 2332	CCCTGGTTG ACTTGCTTCG TCATTAGTT TGCAAAGAAT TGCAATGTCC	400
Consensus	CCCTGGTTG ACTTGCTTCG TCATTAGTT TGCAAAGAAT TGCAATGTCC	400
RespPRRS	GGCGCTACGC GTGTACCAAGA TATAACCAACT TTCTCTGGA CACTAAGGGC	450
VR 2332	GGCGCTACGC GTGTACCAAGA TATAACCAACT TTCTCTGGA CACTAAGGGC	450
Consensus	GGCGCTACGC GTGTACCAAGA TATAACCAACT TTCTCTGGA CACTAAGGGC	450
RespPRRS	GACTCTATC GTTGGGGCTC GGCTCTCATC ATAGAGAAAA CGGGCAAAGT	500
VR 2332	GACTCTATC GTTGGGGCTC GGCTCTCATC ATAGAGAAAA CGGGCAAAGT	500
Consensus	GACTCTATC GTTGGGGCTC GGCTCTCATC ATAGAGAAAA CGGGCAAAGT	500
RespPRRS	TGAGGTCGAA GGTCACTGCA TCGACCTCAA AAGAGTGTG CTTGATGGTT	550
VR 2332	TGAGGTCGAA GGTCACTGCA TCGACCTCAA AAGAGTGTG CTTGATGGTT	550
Consensus	TGAGGTCGAA GGTCACTGCA TCGACCTCAA AAGAGTGTG CTTGATGGTT	550
RespPRRS	CCGTGGCAAC CCCTATAACC AGAGTTCA CGGAACAATG GGTCGTCC	600
VR 2332	CCGTGGCAAC CCCTATAACC AGAGTTCA CGGAACAATG GGTCGTCC	600
Consensus	CCGTGGCAAC CCCTATAACC AGAGTTCA CGGAACAATG GGTCGTCC	600
RespPRRS	TAC	603
VR 2332	TAC	603
Consensus	TAC	603

FIG. 1

RespPRRS	ATGTTGGCAGA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
VR 2332	ATGTTGGCAGA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#1	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#2	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#3	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#4	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#5	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#6	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#7	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#8	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#9	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#10	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#11	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#12	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#13	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#14	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#15	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#16	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#17	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#18	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#19	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
#20	NADC-8	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
NADC-9	ATGTTGCCAA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
Consensus	ATGTTGGDKA	PATGCTTGAC	CCGGGCTCTGT	TGCTTCCCAT	TGCTTTTCTT	50
RespPRRS	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
VR 2332	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#1	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#2	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#3	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#4	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#5	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#6	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#7	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#8	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#9	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#10	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#11	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#12	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#13	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#14	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#15	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#16	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#17	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#18	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#19	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
#20	NADC-8	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
NADC-9	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100
Consensus	CTGGTGTATTC	GTCGGTGTGT	CTTTCCTCTGT	GCTCGGTCAC	GCACAGAACG	100

FIG. 2A

RespPRRS	ACAGCAGCTC	CAATCTCAC	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
VR 2332	ACAGCAGCTC	CAATCTCAC	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#1	ACAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#2	ACAGCAGCTC	CAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#3	ACAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#4	ACAGCAGCTC	TCATCTCCAA	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#5	ACAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#6	CGAGCAGCTC	CAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#7	ACAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#8	CGAGCAGCTC	TCATCTCAC	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#9	ACAGCAGCTC	TCATCTCAC	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#10	CGAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#11	ACAGCAGCTC	TCATCTCAC	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#12	CGAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#13	CGAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#14	ACAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#15	CGAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#16	CGAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#17	ACAGCAGCTC	CAATTCACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#18	CGAGCAGCTC	CAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#19	ACAGCAGCTC	CAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
#20	CGAGCAGCTC	CAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
NADC-8	ACACCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
NADC-9	CGAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150
Consensus	VGAGCAGCTC	AAAATTTACAG	CTGATTTACA	ACGTGACGGCT	ATGTCAGCTG	150

RespPRRS	AATGGCACAG	AAITGCCATAC	TAACAAATT	GAATGGGGCG	TGAGAGCTT	200
VR 2332	AATGGCACAG	AAITGCCATAC	TAACAAATT	GAATGGGGCG	TGAGAGCTT	200
#1	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#2	AATGGCACAG	AAITGCCATAC	TACTAGAATT	GAATGGGGCG	TGAGAGCTT	200
#3	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#4	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#5	AATGGCACAG	AAITGCCATAC	TGATAGAATT	GAATGGGGCG	TGAGAGCTT	200
#6	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#7	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#8	AATGGCACAG	AAITGCCATAC	TGACTAAATT	GAATGGGGCG	TGAGAGCTT	200
#9	AATGGCACAG	AAITGCCATAC	TGATAGAATT	GAATGGGGCG	TGAGAGCTT	200
#10	AATGGCACAG	AAITGCCATAC	TAACAAATT	GAATGGGGCG	TGAGAGCTT	200
#11	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#12	AATGGCACAG	AAITGCCATAC	TGAGAAATT	GAATGGGGCG	TGAGAGCTT	200
#13	AATGGCACAG	AAITGCCATAC	GGGAAAATT	GAATGGGGCG	TGAGAGCTT	200
#14	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#15	AATGGCACAG	AAITGCCATAC	TGACAAGATT	GAATGGGGCG	TGAGAGCTT	200
#16	AATGGCACAG	AAITGCCATAC	TGGGCAATT	GAATGGGGCG	TGAGAGCTT	200
#17	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
#18	AATGGCACAG	AAITGCCATAC	TGATAAAATT	GAATGGGGCG	TGAGAGCTT	200
#19	AATGGCACAG	AAITGCCATAC	TAACAAATT	GAATGGGGCG	TGAGAGCTT	200
#20	AATGGCACAG	AAITGCCATAC	TGACAAATT	GAATGGGGCG	TGAGAGCTT	200
NADC-8	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
NADC-9	AATGGCACAG	AAITGCCATAC	TAATAAATT	GAATGGGGCG	TGAGAGCTT	200
Consensus	AATGGCACAG	AAITGCCATAC	WRRNRRRATT	GATGGGGCG	TGAGAGCTT	200

FIG. 2B

RespPRRS	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
VR 2332	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#1	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#2	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGC	CCCTTACAA	250
#3	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGC	CCCTTACAA	250
#4	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#5	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#6	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#7	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#8	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#9	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#10	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#11	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#12	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#13	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#14	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#15	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#16	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#17	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#18	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#19	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
#20	TGTCACTTTT	CCGTTTGA	CACATTGT	TCTTATGGT	CCCTTACAA	250
NADC-8						
NADC-9						
Consensus	TGTYMMINY	CCGTTTGA	CACATTGT	TCTTATGGY	CCCTTACAA	250

RespPRRS	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
VR 2332	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#1	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#2	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#3	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#4	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#5	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#6	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#7	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#8	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#9	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#10	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#11	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#12	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#13	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#14	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#15	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#16	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#17	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#18	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#19	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
#20	CGGCCATT	CTTGACACA	TTGCTTTC	TCACTGTGTC	AACCGGCGG	300
NADC-8						
NADC-9						
Consensus	CGGCCATT	CTTGACACA	TTGCTTTC	YRYTGTGTC	AACCGGCGG	300

FIG. 2C

RespPRRS	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
VR 2332	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#1	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#2	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#3	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#4	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#5	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#6	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#7	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#8	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#9	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#10	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#11	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#12	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#13	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#14	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#15	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#16	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#17	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#18	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#19	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
#20	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
NADC-8	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
NADC-9	TTTCTTCGCG	GGCGGTATGT	CCTTACAGACC	ATCTAACCGC	TGTGCGCCT	350
Consensus	CTTDKCR	GGGGTATGT	TCATTAAGACC	ATCTAACCGC	TGTGCGCCT	350

RespPRRS	CCCGCGTTG	ACTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
VR 2332	CCCGCGTTG	ACTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#1	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#2	CCCGCGTTG	TTTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#3	CCCGCGTTG	TTTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#4	CCCGCGTTG	ACTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#5	ACCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#6	CCCGCGTTG	TTTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#7	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#8	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#9	CCCGCGTTG	ACTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#10	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#11	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#12	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#13	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#14	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#15	CCCGCGTTG	ACTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#16	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#17	TCCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#18	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#19	CCCGCGTTG	TTTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
#20	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
NADC-8	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
NADC-9	CCCGCGTTG	ATTTGCCTTG	TCATTAAGCTT	GGCAAAACAA	TGCATGTC	400
Consensus	CCCGCGTTG	DTTTCGTYR	TCATTAAGCTT	GGYRAAFAAY	TGCATGTC	400

FIG. 2D

RespPRRS	GGCGCTAACCC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
VR 3312	GGCGCTAACCC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#1	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#2	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#3	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#4	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#5	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#6	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#7	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#8	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#9	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#10	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#11	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#12	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#13	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#14	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#15	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#16	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#17	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#18	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#19	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
#20	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
NADC-8	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
NADC-9	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450
Consensus	GGCGCTAATTC	PTGTAACAGAA	ATATAAACACT	TCTCTCTCGA	CACCAAGGGC	450

RespPRRS	GCACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATAGAIAAAA	GCCCCAAGCT	500
VR 2332	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#1	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#2	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#3	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#4	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#5	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#6	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#7	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#8	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#9	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#10	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAG	GCCCCAAGCT	500
#11	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#12	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#13	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#14	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#15	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAC	GCCCCAAGCT	500
#16	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAC	GCCCCAAGCT	500
#17	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#18	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#19	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
#20	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
NADC-8	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	ATACACAAGAA	GCCCCAAGCT	500
NADC-9	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	CTAGAIAAAA	GCCCCAAGCT	500
Consensus	AGACTCTATC	GTTGGCGCTC	CCCGCTTATC	TCAGAIAARR	RGGGAAAGCT	500

FIG. 2E

RespPRRS	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
VR 2332	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#1	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#2	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#3	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#4	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#5	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#6	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#7	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#8	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#9	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#10	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#11	TCAGGTGCAA GGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#12	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#13	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#14	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#15	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#16	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#17	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#18	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#19	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
#20	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
NADC-8	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
NADC-9	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550
Consensus	TCAGGTGCAA CGTCATCTCA TCGAATTCPA	TAGAGTTGTC CTTGATGGTT	550

RespPRRS	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
VR 2332	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#1	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#2	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#3	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#4	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#5	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#6	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#7	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#8	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#9	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#10	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#11	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#12	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#13	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#14	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#15	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#16	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#17	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#18	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#19	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
#20	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
NADC-8	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
NADC-9	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600
Consensus	CCCTGGOPAC CCCTPTAACC ACGATTTCAG	CGAAACATG GGGTCCTCT	600

FIG. 2F

RespPRRS	TAC	
VR 2332	TAC	603
#1	TAC	603
#2	TAC	603
#3	TAC	603
#4	TAC	603
#5	TAC	603
#6	TAC	603
#7	TAC	603
#8	TAC	603
#9	TAC	603
#10	TAC	603
#11	TAC	603
#12	TAC	603
#13	TAC	603
#14	TAC	603
#15	TAC	603
#16	TAC	603
#17	TAC	603
#18	TAC	603
#19	TAC	603
#20	TAC	603
NADC-8	TAC	603
NADC-9	TAC	603
Consensus	TAC	603

FIG. 2G

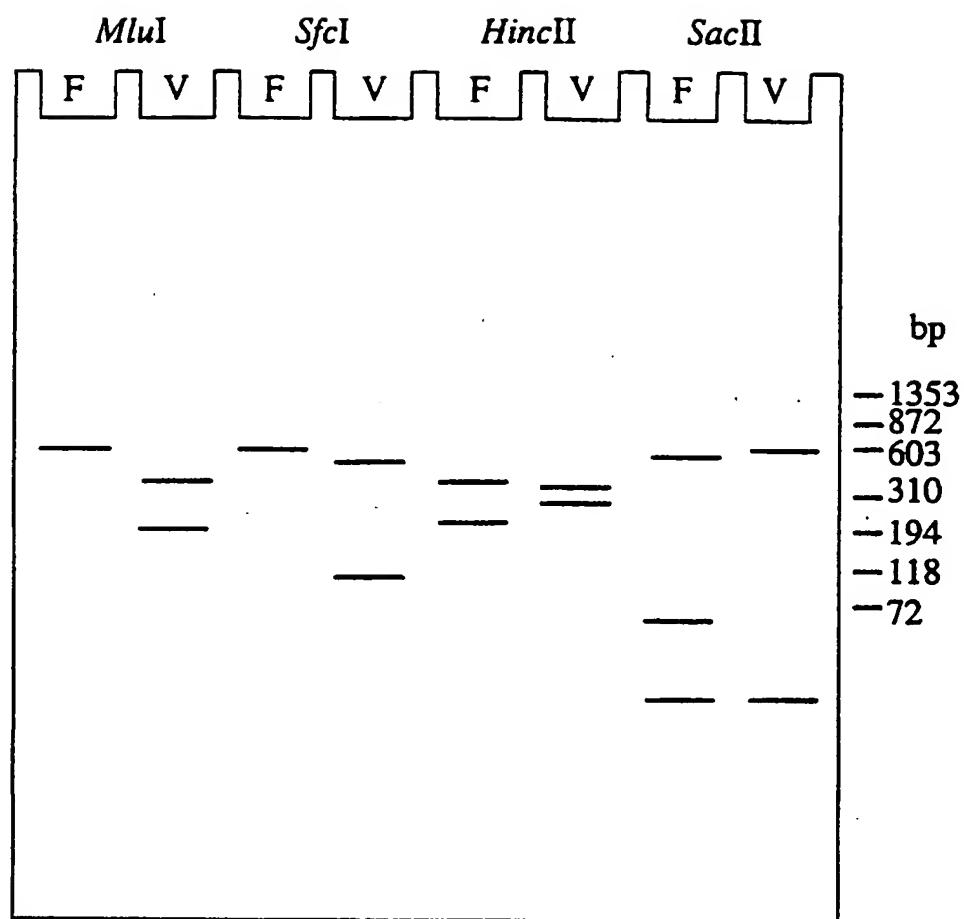


FIG. 3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/03126

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.

US CL :435/106, 108, 109, 110, 115, 235.1, 239; 424/204.1, 218.1, 815

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/106, 108, 109, 110, 115, 235.1, 239; 424/204.1, 218.1, 815

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, CAPLUS, CABA, WPIDS

SEARCH TERMS: LELYSTAD, PRRSV, PEARS, MSD, RESTRICTION ENZYME, CLONE, SEQUENCE, DETECTION, SSLP

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MENG et al. Molecular cloning and nucleotide sequencing of the 3'-terminal genomic RNA of the porcine reproductive and respiratory syndrome virus. Journal of General Virology. 1994. Vol. 75. pages 1795-1801, see entire document.	1-8
Y	KAPUR et al. Genetic variation in porcine reproductive and respiratory syndrome virus isolates in the midwestern United States. Journal of General Virology. 1996. Vol. 77. pages 1271-1276, see entire document.	1-8

Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance		
"E" earlier document published on or after the international filing date	X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	&	document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search	Date of mailing of the international search report
04 JUNE 1997	06.08.97
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer <i>C. Ducke Jr.</i> DANNY LEE
Faxsimile No. (703) 305-3230	Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/03126

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MENG et al. Sequence comparison of open reading frames 2 to 5 of low and high virulence United States isolates of porcine reproductive and respiratory syndrome virus. Journal of General Virology. 1995. Vol. 76. pages 3181-3188, see entire document.	1-8
Y	SUAREZ et al. Direct detection of the porcine reproductive and respiratory syndrome (PRRS) virus by reverse polymerase chain reaction (RT-PCR). Arch. Virol., 1994. Vol. 135. pages 89-99, see entire document.	1-8
Y	WO 92/21375 (STICHTING CENTRAAL DIERGENEESKUNDIG INSTITUUT) 10 December 1992 (10-12-92), see entire document.	1-8
Y	VILGALYS et al. Rapid Genetic Identification and Mapping of Enzymatically Amplified Ribosomal DNA from Several Cryptococcus Species. Journal of Bacteriology. August 1990. Vol. 172, No. 8. pages 4238-4246, see entire document.	1-8
Y	JAYARAO et al. Differentiation of Streptococcus uberis from Streptococcus parauberis by Polymerase Chain Reaction and Restriction Fragment Length Polymorphism Analysis of 16S Ribosomal DNA. Journal of Clinical Microbiology. December 1991. Vol. 29, No. 12. pages 2774-2778, see entire document.	1-8
Y	MARCONI et al. Phylogenetic Analysis of the Genus Borrelia : a Comparison of North american and European Isolates of Borrelia burgdorferi. Journal of Bacteriology. January 1992. Vol. 174, No. 1. pages 241-244, see entire document.	1-8
A	SAITO et al. Characteristics of Major Structural Protein Coding Gene and Leader-Body Sequence in Subgenomic mRNA of Porcine Reproductive and Respiratory Syndrome Virus Isolated in Japan. Journal Vet. Med. Sci. 1996. Vol. 58, No. 4. pages 377-380, see entire document.	1-8
A	MENG et al. Development of a radiolabeled nucleic acid probe for the detection of encephalomyocarditis virus of swine. J. Vet. Diagn. Invest. 1993. Vol. 5. pages 254-258, see entire document.	1-8
A	MARDASSI et al. Identification of major differences in the nucleocapsid protein genes of a Quebec strain and European strains of porcine reproductive and respiratory syndrome virus. Journal of General Virology. March 1994. Vol. 75. pages 681-685, see entire document.	1-8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/03126

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MENG et al. Phylogenetic analyses of the putative M (ORF 6) and N (ORF 7) genes of porcine reproductive and respiratory syndrome virus (PRRSV): implication for the existence of two genotypes of PRRSV in the U.S.A. and Europe. Arch. Virology. 1995, Vol. 140, pages 745-755, see entire document.	1-8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/03126

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

A61K 39/12; C12N 7/00, 7/02; C12P 13/04, 13/24, 13/22, 13/20, 13/14, 13/08